

SEQUENCE LISTING

<110> Mack, David
Gish, Kurt
Wilson, Keith

<120> NOVEL METHODS OF DIAGNOSING CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR CANCER MODULATORS

<130> A-69192-1/DJB/JJD/AMS

<150> US 09/608,821

<151> 2000-06-30

<160> 5

<170> PatentIn version 3.0

<210> 1

<211> 3794

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (38)..(2635)

<400> 1

```

ccaagttcta cctcatgttt ggaggatott gctagct atg gcc ctc gta ctc ggc      55
                                   Met Ala Leu Val Leu Gly
                                   1           5

tcc ctg ttg ctg ctg ggg ctg tgc ggg aac tcc ttt tca gga ggg cag      103
Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn Ser Phe Ser Gly Gly Gln
              10              15              20

cct tca tcc aca gat gct cct aag gct tgg aat tat gaa ttg cct gca      151
Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp Asn Tyr Glu Leu Pro Ala
              25              30              35

aca aat tat gag acc caa gac tcc cat aaa gct gga ccc att ggc att      199
Thr Asn Tyr Glu Thr Gln Asp Ser His Lys Ala Gly Pro Ile Gly Ile
              40              45              50

ctc ttt gaa cta gtg cat atc ttt ctc tat gtg gta cag ccg cgt gat      247
Leu Phe Glu Leu Val His Ile Phe Leu Tyr Val Val Gln Pro Arg Asp
55              60              65              70

ttc cca gaa gat act ttg aga aaa ttc tta cag aag gca tat gaa tcc      295
Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu Gln Lys Ala Tyr Glu Ser
              75              80              85

aaa att gat tat gac aag cca gaa act gta atc tta ggt cta aag att      343
Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val Ile Leu Gly Leu Lys Ile
              90              95              100

gtc tac tat gaa gca ggg att att cta tgc tgt gtc ctg ggg ctg ctg      391
Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys Cys Val Leu Gly Leu Leu
              105              110              115

ttt att att ctg atg cct ctg gtg ggg tat ttc ttt tgt atg tgt cgt      439

```

Phe	Ile	Ile	Leu	Met	Pro	Leu	Val	Gly	Tyr	Phe	Phe	Cys	Met	Cys	Arg		
120						125					130						
tgc	tgt	aac	aaa	tgt	ggc	gga	gaa	atg	cac	cag	cga	cag	aag	gaa	aat	487	
Cys	Cys	Asn	Lys	Cys	Gly	Gly	Glu	Met	His	Gln	Arg	Gln	Lys	Glu	Asn		
135					140					145					150		
ggg	ccc	ttc	ctg	agg	aaa	tgc	ttt	gca	atc	tcc	ctg	ttg	gtg	att	tgt	535	
Gly	Pro	Phe	Leu		Lys	Cys	Phe	Ala	Ile	Ser	Leu	Leu	Val	Ile	Cys		
				155					160					165			
ata	ata	ata	agc	att	ggc	atc	ttc	tat	ggc	ttt	gtg	gca	aat	cac	cag	583	
Ile	Ile	Ile	Ser	Ile	Gly	Ile	Phe	Tyr	Gly	Phe	Val	Ala	Asn	His	Gln		
			170					175					180				
gta	aga	acc	cgg	atc	aaa	agg	agt	cgg	aaa	ctg	gca	gat	agc	aat	ttc	631	
Val	Arg	Thr	Arg	Ile	Lys	Arg	Ser	Arg	Lys	Leu	Ala	Asp	Ser	Asn	Phe		
			185				190					195					
aag	gac	ttg	cga	act	ctc	ttg	aat	gaa	act	cca	gag	caa	atc	aaa	tat	679	
Lys	Asp	Leu	Arg	Thr	Leu	Leu	Asn	Glu	Thr	Pro	Glu	Gln	Ile	Lys	Tyr		
	200					205					210						
ata	ttg	gcc	cag	tac	aac	act	acc	aag	gac	aag	gcg	ttc	aca	gat	ctg	727	
Ile	Leu	Ala	Gln	Tyr	Asn	Thr	Thr	Lys	Asp	Lys	Ala	Phe	Thr	Asp	Leu		
	215				220					225					230		
aac	agt	atc	aat	tca	gtg	cta	gga	ggc	gga	att	ctt	gac	cga	ctg	aga	775	
Asn	Ser	Ile	Asn	Ser	Val	Leu	Gly	Gly	Gly	Ile	Leu	Asp	Arg	Leu	Arg		
			235					240						245			
ccc	aac	atc	atc	cct	gtt	ctt	gat	gag	att	aag	tcc	atg	gca	aca	gcg	823	
Pro	Asn	Ile	Ile	Pro	Val	Leu	Asp	Glu	Ile	Lys	Ser	Met	Ala	Thr	Ala		
			250					255					260				
atc	aag	gag	acc	aaa	gag	gcg	ttg	gag	aac	atg	aac	agc	acc	ttg	aag	871	
Ile	Lys	Glu	Thr	Lys	Glu	Ala	Leu	Glu	Asn	Met	Asn	Ser	Thr	Leu	Lys		
		265					270					275					
agc	ttg	cac	caa	caa	agt	aca	cag	ctt	agc	agc	agt	ctg	acc	agc	gtg	919	
Ser	Leu	His	Gln	Gln	Ser	Thr	Gln	Leu	Ser	Ser	Ser	Leu	Thr	Ser	Val		
	280					285				290							
aaa	act	agc	ctg	cgg	tca	tct	ctc	aat	gac	cct	ctg	tgc	ttg	gtg	cat	967	
Lys	Thr	Ser	Leu	Arg	Ser	Ser	Leu	Asn	Asp	Pro	Leu	Cys	Leu	Val	His		
	295				300					305					310		
cca	tca	agt	gaa	acc	tgc	aac	agc	atc	aga	ttg	tct	cta	agc	cag	ctg	1015	
Pro	Ser	Ser	Glu	Thr	Cys	Asn	Ser	Ile	Arg	Leu	Ser	Leu	Ser	Gln	Leu		
				315					320					325			
aat	agc	aac	cct	gaa	ctg	agg	cag	ctt	cca	ccc	gtg	gat	gca	gaa	ctt	1063	
Asn	Ser	Asn	Pro	Glu	Leu	Arg	Gln	Leu	Pro	Pro	Val	Asp	Ala	Glu	Leu		
			330					335					340				
gac	aac	gtt	aat	aac	gtt	ctt	agg	aca	gat	ttg	gat	ggc	ctg	gtc	caa	1111	
Asp	Asn	Val	Asn	Asn	Val	Leu	Arg	Thr	Asp	Leu	Asp	Gly	Leu	Val	Gln		
		345				350						355					
cag	ggc	tat	caa	tcc	ctt	aat	gat	ata	cct	gac	aga	gta	caa	cgc	caa	1159	
Gln	Gly	Tyr	Gln	Ser	Leu	Asn	Asp	Ile	Pro	Asp	Arg	Val	Gln	Arg	Gln		

aga aaa aac ctt cag gat ttt gct gct tgt gga ata gac aga atg aat	1927
Arg Lys Asn Leu Gln Asp Phe Ala Ala Cys Gly Ile Asp Arg Met Asn	
615 620 625 630	
tat gac agc tac ttg gct cag act ggt aaa tcc ccc gca gga gtg aat	1975
Tyr Asp Ser Tyr Leu Ala Gln Thr Gly Lys Ser Pro Ala Gly Val Asn	
635 640 645	
ctt tta tca ttt gca tat gat cta gaa gca aaa gca aac agt ttg ccc	2023
Leu Leu Ser Phe Ala Tyr Asp Leu Glu Ala Lys Ala Asn Ser Leu Pro	
650 655 660	
cca gga aat ttg agg aac tcc ctg aaa aga gat gca caa act att aaa	2071
Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys	
665 670 675	
aca att cac cag caa cga gtc ctt cct ata gaa caa tca ctg agc act	2119
Thr Ile His Gln Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr	
680 685 690	
cta tac caa agc gtc aag ata ctt caa cgc aca ggg aat gga ttg ttg	2167
Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu	
695 700 705 710	
gag aga gta act agg att cta gct tct ctg gat ttt gct cag aac ttc	2215
Glu Arg Val Thr Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe	
715 720 725	
atc aca aac aat act tcc tct gtt att att gag gaa act aag aag tat	2263
Ile Thr Asn Asn Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr	
730 735 740	
ggg aga aca ata ata gga tat ttt gaa cat tat ctg cag tgg atc gag	2311
Gly Arg Thr Ile Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu	
745 750 755	
ttc tct atc agt gag aaa gtg gca tcg tgc aaa cct gtg gcc acc gct	2359
Phe Ser Ile Ser Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala	
760 765 770	
cta gat act gct gtt gat gtc ttt ctg tgt agc tac att atc gac ccc	2407
Leu Asp Thr Ala Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro	
775 780 785 790	
ttg aat ttg ttt tgg ttt ggc ata gga aaa gct act gta ttt tta ctt	2455
Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu	
795 800 805	
ccg gct cta att ttt gcg gta aaa ctg gct aag tac tat cgt cga atg	2503
Pro Ala Leu Ile Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met	
810 815 820	
gat tcg gag gac gtg tac gat gat gtt gaa act ata ccc atg aaa aat	2551
Asp Ser Glu Asp Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn	
825 830 835	
atg gaa aat ggt aat aat ggt tat cat aaa gat cat gta tat ggt att	2599
Met Glu Asn Gly Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile	
840 845 850	

cac aat cct gtt atg aca agc cca tca caa cat tga tagctgatgt 2645
 His Asn Pro Val Met Thr Ser Pro Ser Gln His
 855 860 865
 tgaaactgct tgagcatcag gatactcaaa gtggaaagga tcacagattt ttggtagttt 2705
 ctgggtctac aaggactttc caaatccagg agcaacgccca gtggcaacgt agtgactcag 2765
 gcgggcacca aggcaacggc accattggtc tctgggtagt gctttaagaa tgaacacaat 2825
 cacgttatag tccatgggtcc atcactattc aaggatgact ccctcccttc ctgtctattt 2885
 ttgtttttta cttttttaca ctgagtttct atttagacac tacaacatat ggggtgtttg 2945
 ttcccattgg atgcatttct atcaaaaactc tatcaaatgt gatggctaga ttctaacata 3005
 ttgccatgtg tggagtgtgc tgaacacaca ccagtttaca ggaaagatgc attttgtgta 3065
 cagtaaacgg tgtatatacc ttttgttacc acagagtttt ttaaacaat gagtattata 3125
 ggactttctt ctaaatgagc taaataagtc accattgact tcttggtgct gttgaaaata 3185
 atccattttc actaaaagtg tgtgaaacct acagcatatt cttcacgcag agattttcat 3245
 ctattatact ttatcaaaga ttggccatgt tccacttggg aatggcatgc aaaagccatc 3305
 atagagaaac ctgcgtaact ccatctgaca aattcaaaag agagagagag atcttgagag 3365
 agaaatgctg ttcgttcaaa agtggagttg ttttaacaga tgccaattac ggtgtacagt 3425
 ttaacagagt tttctgttgc attaggataa acattaattg gagtgcagct aacatgagta 3485
 tcatcagact agtatcaagt gttctaaaat gaaatatgag aagatcctgt cacaattctt 3545
 agatctggtg tccagcatgg atgaaacctt tgagtttggg ccctaaattt gcatgaaagc 3605
 acaaggtaaa tattcatttg cttcaggagt ttcatgttgg atctgtcatt atcaaaagtg 3665
 atcagcaatg aagaactggg cggacaaaat ttaacgttga tgtaatggaa ttccagatgt 3725
 aggcattccc cccaggtctt ttcatgtgca gattgcagtt ctgattcatt tgaataaaaa 3785
 ggaacttgg 3794

<210> 2
 <211> 865
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Ala Leu Val Leu Gly Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn
 1 5 10 15

Ser Phe Ser Gly Gly Gln Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp
 20 25 30

Asn Tyr Glu Leu Pro Ala Thr Asn Tyr Glu Thr Gln Asp Ser His Lys

35

40

45

Ala Gly Pro Ile Gly Ile Leu Phe Glu Leu Val His Ile Phe Leu Tyr
50 55 60

Val Val Gln Pro Arg Asp Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu
65 70 75 80

Gln Lys Ala Tyr Glu Ser Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val
85 90 95

Ile Leu Gly Leu Lys Ile Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys
100 105 110

Cys Val Leu Gly Leu Leu Phe Ile Ile Leu Met Pro Leu Val Gly Tyr
115 120 125

Phe Phe Cys Met Cys Arg Cys Cys Asn Lys Cys Gly Gly Glu Met His
130 135 140

Gln Arg Gln Lys Glu Asn Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile
145 150 155 160

Ser Leu Leu Val Ile Cys Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly
165 170 175

Phe Val Ala Asn His Gln Val Arg Thr Arg Ile Lys Arg Ser Arg Lys
180 185 190

Leu Ala Asp Ser Asn Phe Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr
195 200 205

Pro Glu Gln Ile Lys Tyr Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp
210 215 220

Lys Ala Phe Thr Asp Leu Asn Ser Ile Asn Ser Val Leu Gly Gly Gly
225 230 235 240

Ile Leu Asp Arg Leu Arg Pro Asn Ile Ile Pro Val Leu Asp Glu Ile
245 250 255

Lys Ser Met Ala Thr Ala Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn
260 265 270

Met Asn Ser Thr Leu Lys Ser Leu His Gln Gln Ser Thr Gln Leu Ser
275 280 285

Ser Ser Leu Thr Ser Val Lys Thr Ser Leu Arg Ser Ser Leu Asn Asp
 290 295 300

Pro Leu Cys Leu Val His Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg
 305 310 315 320

Leu Ser Leu Ser Gln Leu Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro
 325 330 335

Pro Val Asp Ala Glu Leu Asp Asn Val Asn Asn Val Leu Arg Thr Asp
 340 345 350

Leu Asp Gly Leu Val Gln Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro
 355 360 365

Asp Arg Val Gln Arg Gln Thr Thr Thr Val Val Ala Gly Ile Lys Arg
 370 375 380

Val Leu Asn Ser Ile Gly Ser Asp Ile Asp Asn Val Thr Gln Arg Leu
 385 390 395 400

Pro Ile Gln Asp Ile Leu Ser Ala Phe Ser Val Tyr Val Asn Asn Thr
 405 410 415

Glu Ser Tyr Ile His Arg Asn Leu Pro Thr Leu Glu Glu Tyr Asp Ser
 420 425 430

Tyr Trp Trp Leu Gly Gly Leu Val Ile Cys Ser Leu Leu Thr Leu Ile
 435 440 445

Val Ile Phe Tyr Tyr Leu Gly Leu Leu Cys Gly Val Cys Gly Tyr Asp
 450 455 460

Arg His Ala Thr Pro Thr Thr Arg Gly Cys Val Ser Asn Thr Gly Gly
 465 470 475 480

Val Phe Leu Met Val Gly Val Gly Leu Ser Phe Leu Phe Cys Trp Ile
 485 490 495

Leu Met Ile Ile Val Val Leu Thr Phe Val Phe Gly Ala Asn Val Glu
 500 505 510

Lys Leu Ile Cys Glu Pro Tyr Thr Ser Lys Glu Leu Phe Arg Val Leu
 515 520 525

Asp Thr Pro Tyr Leu Leu Asn Glu Asp Trp Glu Tyr Tyr Leu Ser Gly
530 535 540

Lys Leu Phe Asn Lys Ser Lys Met Lys Leu Thr Phe Glu Gln Val Tyr
545 550 555 560

Ser Asp Cys Lys Lys Asn Arg Gly Thr Tyr Gly Thr Leu His Leu Gln
565 570 575

Asn Ser Phe Asn Ile Ser Glu His Leu Asn Ile Asn Glu His Thr Gly
580 585 590

Ser Ile Ser Ser Glu Leu Glu Ser Leu Lys Val Asn Leu Asn Ile Phe
595 600 605

Leu Leu Gly Ala Ala Gly Arg Lys Asn Leu Gln Asp Phe Ala Ala Cys
610 615 620

Gly Ile Asp Arg Met Asn Tyr Asp Ser Tyr Leu Ala Gln Thr Gly Lys
625 630 635 640

Ser Pro Ala Gly Val Asn Leu Leu Ser Phe Ala Tyr Asp Leu Glu Ala
645 650 655

Lys Ala Asn Ser Leu Pro Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg
660 665 670

Asp Ala Gln Thr Ile Lys Thr Ile His Gln Gln Arg Val Leu Pro Ile
675 680 685

Glu Gln Ser Leu Ser Thr Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg
690 695 700

Thr Gly Asn Gly Leu Leu Glu Arg Val Thr Arg Ile Leu Ala Ser Leu
705 710 715 720

Asp Phe Ala Gln Asn Phe Ile Thr Asn Asn Thr Ser Ser Val Ile Ile
725 730 735

Glu Glu Thr Lys Lys Tyr Gly Arg Thr Ile Ile Gly Tyr Phe Glu His
740 745 750

Tyr Leu Gln Trp Ile Glu Phe Ser Ile Ser Glu Lys Val Ala Ser Cys
755 760 765

Lys Pro Val Ala Thr Ala Leu Asp Thr Ala Val Asp Val Phe Leu Cys
770 775 780

Ser Tyr Ile Ile Asp Pro Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys
785 790 795 800

Ala Thr Val Phe Leu Leu Pro Ala Leu Ile Phe Ala Val Lys Leu Ala
805 810 815

Lys Tyr Tyr Arg Arg Met Asp Ser Glu Asp Val Tyr Asp Asp Val Glu
820 825 830

Thr Ile Pro Met Lys Asn Met Glu Asn Gly Asn Asn Gly Tyr His Lys
835 840 845

Asp His Val Tyr Gly Ile His Asn Pro Val Met Thr Ser Pro Ser Gln
850 855 860

His
865

<210> 3
<211> 3764
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (38) .. (2605)

<400> 3
ccaagttcta cctcatgttt ggaggatctt gctagct atg gcc ctc gta ctc ggc 55
Met Ala Leu Val Leu Gly
1 5

tcc ctg ttg ctg ctg ggg ctg tgc ggg aac tcc ttt tca gga ggg cag 103
Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn Ser Phe Ser Gly Gly Gln
10 15 20

cct tca tcc aca gat gct cct aag gct tgg aat tat gaa ttg cct gca 151
Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp Asn Tyr Glu Leu Pro Ala
25 30 35

aca aat tat gag acc caa gac tcc cat aaa gct gga ccc att ggc att 199
Thr Asn Tyr Glu Thr Gln Asp Ser His Lys Ala Gly Pro Ile Gly Ile
40 45 50

ctc ttt gaa cta gtg cat atc ttt ctc tat gtg gta cag ccg cgt gat 247
Leu Phe Glu Leu Val His Ile Phe Leu Tyr Val Val Gln Pro Arg Asp
55 60 65 70

ttc cca gaa gat act ttg aga aaa ttc tta cag aag gca tat gaa tcc 295
Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu Gln Lys Ala Tyr Glu Ser
75 80 85

aaa att gat tat gac att gtc tac tat gaa gca ggg att att cta tgc	343
Lys Ile Asp Tyr Asp Ile Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys	
90 95 100	
tgt gtc ctg ggg ctg ctg ttt att att ctg atg cct ctg gtg ggg tat	391
Cys Val Leu Gly Leu Leu Phe Ile Ile Leu Met Pro Leu Val Gly Tyr	
105 110 115	
ttc ttt tgt atg tgt cgt tgc tgt aac aaa tgt ggt gga gaa atg cac	439
Phe Phe Cys Met Cys Arg Cys Cys Asn Lys Cys Gly Gly Glu Met His	
120 125 130	
cag cga cag aag gaa aat ggg ccc ttc ctg agg aaa tgc ttt gca atc	487
Gln Arg Gln Lys Glu Asn Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile	
135 140 145 150	
tcc ctg ttg gtg att tgt ata ata ata agc att ggc atc ttc tat ggt	535
Ser Leu Leu Val Ile Cys Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly	
155 160 165	
ttt gtg gca aat cac cag gta aga acc cgg atc aaa agg agt cgg aaa	583
Phe Val Ala Asn His Gln Val Arg Thr Arg Ile Lys Arg Ser Arg Lys	
170 175 180	
ctg gca gat agc aat ttc aag gac ttg cga act ctc ttg aat gaa act	631
Leu Ala Asp Ser Asn Phe Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr	
185 190 195	
cca gag caa atc aaa tat ata ttg gcc cag tac aac act acc aag gac	679
Pro Glu Gln Ile Lys Tyr Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp	
200 205 210	
aag gcg ttc aca gat ctg aac agt atc aat tca gtg cta gga ggc gga	727
Lys Ala Phe Thr Asp Leu Asn Ser Ile Asn Ser Val Leu Gly Gly Gly	
215 220 225 230	
att ctt gac cga ctg aga ccc aac atc atc cct gtt ctt gat gag att	775
Ile Leu Asp Arg Leu Arg Pro Asn Ile Ile Pro Val Leu Asp Glu Ile	
235 240 245	
aag tcc atg gca aca gcg atc aag gag acc aaa gag gcg ttg gag aac	823
Lys Ser Met Ala Thr Ala Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn	
250 255 260	
atg aac agc acc ttg aag agc ttg cac caa caa agt aca cag ctt agc	871
Met Asn Ser Thr Leu Lys Ser Leu His Gln Gln Ser Thr Gln Leu Ser	
265 270 275	
agc agt ctg acc agc gtg aaa act agc ctg cgg tca tct ctc aat gac	919
Ser Ser Leu Thr Ser Val Lys Thr Ser Leu Arg Ser Ser Leu Asn Asp	
280 285 290	
cct ctg tgc ttg gtg cat cca tca agt gaa acc tgc aac agc atc aga	967
Pro Leu Cys Leu Val His Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg	
295 300 305 310	
ttg tct cta agc cag ctg aat agc aac cct gaa ctg agg cag ctt cca	1015
Leu Ser Leu Ser Gln Leu Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro	
315 320 325	

ccc gtg gat gca gaa ctt gac aac gtt aat aac gtt ctt agg aca gat	1063
Pro Val Asp Ala Glu Leu Asp Asn Val Asn Asn Val Leu Arg Thr Asp	
330 335 340	
ttg gat ggc ctg gtc caa cag ggc tat caa tcc ctt aat gat ata cct	1111
Leu Asp Gly Leu Val Gln Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro	
345 350 355	
gac aga gta caa cgc caa acc acg act gtc gta gca ggt atc aaa agg	1159
Asp Arg Val Gln Arg Gln Thr Thr Val Val Ala Gly Ile Lys Arg	
360 365 370	
gtc ttg aat tcc att ggt tca gat atc gac aat gta act cag cgt ctt	1207
Val Leu Asn Ser Ile Gly Ser Asp Ile Asp Asn Val Thr Gln Arg Leu	
375 380 385 390	
cct att cag gat ata ctc tca gca ttc tct gtt tat gtt aat aac act	1255
Pro Ile Gln Asp Ile Leu Ser Ala Phe Ser Val Tyr Val Asn Asn Thr	
395 400 405	
gaa agt tac atc cac aga aat tta cct aca ttg gaa gag tat gat tca	1303
Glu Ser Tyr Ile His Arg Asn Leu Pro Thr Leu Glu Glu Tyr Asp Ser	
410 415 420	
tac tgg tgg ctg ggt ggc ctg gtc atc tgc tct ctg ctg acc ctc atc	1351
Tyr Trp Trp Leu Gly Gly Leu Val Ile Cys Ser Leu Leu Thr Leu Ile	
425 430 435	
gtg att ttt tac tac ctg ggc tta ctg tgt ggc gtg tgc ggc tat gac	1399
Val Ile Phe Tyr Tyr Leu Gly Leu Leu Cys Gly Val Cys Gly Tyr Asp	
440 445 450	
agg cat gcc acc ccg acc acc cga ggc tgt gtc tcc aac acc gga ggc	1447
Arg His Ala Thr Pro Thr Thr Arg Gly Cys Val Ser Asn Thr Gly Gly	
455 460 465 470	
gtc ttc ctc atg gtt gga gtt gga tta agt ttc ctc ttt tgc tgg ata	1495
Val Phe Leu Met Val Gly Val Gly Leu Ser Phe Leu Phe Cys Trp Ile	
475 480 485	
ttg atg atc att gtg gtt ctt acc ttt gtc ttt ggt gca aat gtg gaa	1543
Leu Met Ile Ile Val Val Leu Thr Phe Val Phe Gly Ala Asn Val Glu	
490 495 500	
aaa ctg atc tgt gaa cct tac acg agc aag gaa tta ttc cgg gtt ttg	1591
Lys Leu Ile Cys Glu Pro Tyr Thr Ser Lys Glu Leu Phe Arg Val Leu	
505 510 515	
gat aca ccc tac tta cta aat gaa gac tgg gaa tac tat ctc tct ggg	1639
Asp Thr Pro Tyr Leu Leu Asn Glu Asp Trp Glu Tyr Tyr Leu Ser Gly	
520 525 530	
aag cta ttt aat aaa tca aaa atg aag ctc act ttt gaa caa gtt tac	1687
Lys Leu Phe Asn Lys Ser Lys Met Lys Leu Thr Phe Glu Gln Val Tyr	
535 540 545 550	
agt gac tgc aaa aaa aat aga ggc act tac ggc act ctt cac ctg cag	1735
Ser Asp Cys Lys Lys Asn Arg Gly Thr Tyr Gly Thr Leu His Leu Gln	
555 560 565	
aac agc ttc aat atc agt gaa cat ctc aac att aat gag cat act gga	1783

Asn Ser Phe Asn Ile Ser Glu His Leu Asn Ile Asn Glu His Thr Gly	
570 575 580	
agc ata agc agt gaa ttg gaa agt ctg aag gta aat ctt aat atc ttt	1831
Ser Ile Ser Ser Glu Leu Glu Ser Leu Lys Val Asn Leu Asn Ile Phe	
585 590 595	
ctg ttg ggt gca gca gga aga aaa aac ctt cag gat ttt gct gct tgt	1879
Leu Leu Gly Ala Ala Gly Arg Lys Asn Leu Gln Asp Phe Ala Ala Cys	
600 605 610	
gga ata gac aga atg aat tat gac agc tac ttg gct cag act ggt aaa	1927
Gly Ile Asp Arg Met Asn Tyr Asp Ser Tyr Leu Ala Gln Thr Gly Lys	
615 620 625 630	
tcc ccc gca gga gtg aat ctt tta tca ttt gca tat gat cta gaa gca	1975
Ser Pro Ala Gly Val Asn Leu Leu Ser Phe Ala Tyr Asp Leu Ala Ala	
635 640 645	
aaa gca aac agt ttg ccc cca gga aat ttg agg aac tcc ctg aaa aga	2023
Lys Ala Asn Ser Leu Pro Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg	
650 655 660	
gat gca caa act att aaa aca att cac cag caa cga gtc ctt cct ata	2071
Asp Ala Gln Thr Ile Lys Thr Ile His Gln Gln Arg Val Leu Pro Ile	
665 670 675	
gaa caa tca ctg agc act cta tac caa agc gtc aag ata ctt caa cgc	2119
Glu Gln Ser Leu Ser Thr Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg	
680 685 690	
aca ggg aat gga ttg ttg gag aga gta act agg att cta gct tct ctg	2167
Thr Gly Asn Gly Leu Leu Glu Arg Val Thr Arg Ile Leu Ala Ser Leu	
695 700 705 710	
gat ttt gct cag aac ttc atc aca aac aat act tcc tct gtt att att	2215
Asp Phe Ala Gln Asn Phe Ile Thr Asn Asn Thr Ser Ser Val Ile Ile	
715 720 725	
gag gaa act aag aag tat ggg aga aca ata ata gga tat ttt gaa cat	2263
Glu Glu Thr Lys Lys Tyr Gly Arg Thr Ile Ile Gly Tyr Phe Glu His	
730 735 740	
tat ctg cag tgg atc gag ttc tct atc agt gag aaa gtg gca tcg tgc	2311
Tyr Leu Gln Trp Ile Glu Phe Ser Ile Ser Glu Lys Val Ala Ser Cys	
745 750 755	
aaa cct gtg gcc acc gct cta gat act gct gtt gat gtc ttt ctg tgt	2359
Lys Pro Val Ala Thr Ala Leu Asp Thr Ala Val Asp Val Phe Leu Cys	
760 765 770	
agc tac att atc gac ccc ttg aat ttg ttt tgg ttt ggc ata gga aaa	2407
Ser Tyr Ile Ile Asp Pro Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys	
775 780 785 790	
gct act gta ttt tta ctt ccg gct cta att ttt gcg gta aaa ctg gct	2455
Ala Thr Val Phe Leu Leu Pro Ala Leu Ile Phe Ala Val Lys Leu Ala	
795 800 805	
aag tac tat cgt cga atg gat tcg gag gac gtg tac gat gat gtt gaa	2503
Lys Tyr Tyr Arg Arg Met Asp Ser Glu Asp Val Tyr Asp Asp Val Glu	

810					815					820						
act	ata	ccc	atg	aaa	aat	atg	gaa	aat	ggt	aat	aat	ggt	tat	cat	aaa	2551
Thr	Ile	Pro	Met	Lys	Asn	Met	Glu	Asn	Gly	Asn	Asn	Gly	Tyr	His	Lys	
825					830					835						
gat	cat	gta	tat	ggt	att	cac	aat	cct	ggt	atg	aca	agc	cca	tca	caa	2599
Asp	His	Val	Tyr	Gly	Ile	His	Asn	Pro	Val	Met	Thr	Ser	Pro	Ser	Gln	
840					845					850						
cat	tga	tagctgatgt	tgaaaactgct	tgagcatcag	gataactcaaa					gtggaaagga					2655	
His																
855																
tcacagattt	ttggtagttt	ctgggtctac	aaggactttc	caaatccagg	agcaacgccca										2715	
gtggcaacgt	agtgactcag	gcgggcacca	aggcaacggc	accattgggc	tctgggtagt										2775	
gctttaagaa	tgaacacaat	cacgttatag	tccatgggcc	atcactattc	aaggatgact										2835	
ccctcccttc	ctgtctattt	ttgtttttta	ctttttttaca	ctgagtttct	atttagacac										2895	
tacaacatat	ggggtgtttg	ttcccatagg	atgcatttct	atcaaaaactc	tatcaaatgt										2955	
gatggctaga	ttctaacata	ttgccatgtg	tggagtgtgc	tgaacacaca	ccagtttaca										3015	
ggaaagatgc	attttgtgta	cagtaaaacgg	tgtatataacc	ttttgttacc	acagagtttt										3075	
ttaaacaaat	gagtattata	ggacttttctt	ctaaatgagc	taaataagtc	accattgact										3135	
tcttggtgct	gttgaaaata	atccattttc	actaaaagtg	tgtgaaacct	acagcatatt										3195	
cttcacgcag	agattttcat	ctattatact	ttatcaaaga	ttggccatgt	tccacttgga										3255	
aatggcatgc	aaaagccatc	atagagaaaac	ctgcgttaact	ccatctgaca	aattcaaaaag										3315	
agagagagag	atcttgagag	agaaatgctg	ttcgttcaaa	agtggagttg	ttttaacaga										3375	
tgccaattac	ggtgtacagt	ttaacagagt	tttctgttgc	attaggataa	acattaattg										3435	
gagtgcagct	aacatgagta	tcatcagact	agtatcaagt	gttctaaaat	gaaatatgag										3495	
aagatcctgt	cacaattctt	agatctgggtg	tccagcatgg	atgaaacctt	tgagtttggt										3555	
ccctaaattt	gcatgaaagc	acaaggtaaa	tattcatttg	cttcaggagt	ttcatgttgg										3615	
atctgtcatt	atcaaaaagtg	atcagcaatg	aagaactggg	cggacaaaat	ttaacgttga										3675	
tgtaatggaa	ttccagatgt	aggcattccc	cccaggctctt	ttcatgtgca	gattgcagtt										3735	
ctgatttcatt	tgaataaaaaa	ggaacttgg												3764		

```
<210> 4
<211> 855
<212> PRT
<213> Homo sapiens
```

Met Ala Leu Val Leu Gly Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn

[illegible]

Lys Glu Ala Leu Glu Asn Met Asn Ser Thr Leu Lys Ser Leu His Gln
 260 265 270

Gln Ser Thr Gln Leu Ser Ser Ser Leu Thr Ser Val Lys Thr Ser Leu
 275 280 285

Arg Ser Ser Leu Asn Asp Pro Leu Cys Leu Val His Pro Ser Ser Glu
 290 295 300

Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu Asn Ser Asn Pro
 305 310 315 320

Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu Asp Asn Val Asn
 325 330 335

Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln Gln Gly Tyr Gln
 340 345 350

Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln Thr Thr Thr Val
 355 360 365

Val Ala Gly Ile Lys Arg Val Leu Asn Ser Ile Gly Ser Asp Ile Asp
 370 375 380

Asn Val Thr Gln Arg Leu Pro Ile Gln Asp Ile Leu Ser Ala Phe Ser
 385 390 395 400

Val Tyr Val Asn Asn Thr Glu Ser Tyr Ile His Arg Asn Leu Pro Thr
 405 410 415

Leu Glu Glu Tyr Asp Ser Tyr Trp Trp Leu Gly Gly Leu Val Ile Cys
 420 425 430

Ser Leu Leu Thr Leu Ile Val Ile Phe Tyr Tyr Leu Gly Leu Leu Cys
 435 440 445

Gly Val Cys Gly Tyr Asp Arg His Ala Thr Pro Thr Thr Arg Gly Cys
 450 455 460

Val Ser Asn Thr Gly Gly Val Phe Leu Met Val Gly Val Gly Leu Ser
 465 470 475 480

Phe Leu Phe Cys Trp Ile Leu Met Ile Ile Val Val Leu Thr Phe Val
 485 490 495

Phe Gly Ala Asn Val Glu Lys Leu Ile Cys Glu Pro Tyr Thr Ser Lys
500 505 510

Glu Leu Phe Arg Val Leu Asp Thr Pro Tyr Leu Leu Asn Glu Asp Trp
515 520 525

Glu Tyr Tyr Leu Ser Gly Lys Leu Phe Asn Lys Ser Lys Met Lys Leu
530 535 540

Thr Phe Glu Gln Val Tyr Ser Asp Cys Lys Lys Asn Arg Gly Thr Tyr
545 550 555 560

Gly Thr Leu His Leu Gln Asn Ser Phe Asn Ile Ser Glu His Leu Asn
565 570 575

Ile Asn Glu His Thr Gly Ser Ile Ser Ser Glu Leu Glu Ser Leu Lys
580 585 590

Val Asn Leu Asn Ile Phe Leu Leu Gly Ala Ala Gly Arg Lys Asn Leu
595 600 605

Gln Asp Phe Ala Ala Cys Gly Ile Asp Arg Met Asn Tyr Asp Ser Tyr
610 615 620

Leu Ala Gln Thr Gly Lys Ser Pro Ala Gly Val Asn Leu Leu Ser Phe
625 630 635 640

Ala Tyr Asp Leu Glu Ala Lys Ala Asn Ser Leu Pro Pro Gly Asn Leu
645 650 655

Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys Thr Ile His Gln
660 665 670

Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr Leu Tyr Gln Ser
675 680 685

Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu Glu Arg Val Thr
690 695 700

Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe Ile Thr Asn Asn
705 710 715 720

Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr Gly Arg Thr Ile
725 730 735

Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu Phe Ser Ile Ser
740 745 750

Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala Leu Asp Thr Ala
755 760 765

Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro Leu Asn Leu Phe
770 775 780

Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu Pro Ala Leu Ile
785 790 795 800

Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met Asp Ser Glu Asp
805 810 815

Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn Met Glu Asn Gly
820 825 830

Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile His Asn Pro Val
835 840 845

Met Thr Ser Pro Ser Gln His
850 855

<210> 5
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Extracellular cytokine receptor motif found in many species.

<220>
<221> UNSURE
<222> (3)..(3)
<223> "Xaa" at position 3 can be any amino acid.

<400> 5

Trp Ser Xaa Trp Ser
1 5